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Bayesian Inference for Discretely Observed Diffusion Epidemic Model

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Abstract

Most epidemic data are discretely observed at irregular-time interval subject to environmental influence. No doubt, the dynamic of such epidemic data can be well described by discretely observed method of estimation. However, parameter estimation under such process proves to be challenging in practice. The challenges normally encounter are generally in the intractability of the transition densities, resulting into the likelihood functions which are not in closed form. Direct implementation of classical method of statistical estimation often results into convergences problems. Indeed, literatures have not adequately addressed such challenges in practice. To this end, this article is design to examining and address the estimation problems which is usually plagued with convergences. We adopted Bayesian data-augmentation method of parameters estimation for such problems. The proposed method is applied to simulation dataset. Results obtained encourage that this method of parameters estimate has ability to solve challenges encounters in the literature.

1. INTRODUCTION

Most epidemic data are discretely observed and undergo stochastic transition rate. Stochastic epidemic models allow more realistic description of the transmission of disease as compared to deterministic epidemic models [1-3]. However, parameter estimation is challenging for discretely observed data under stochastic models [4,5]. Several methods of frequentist procedures to infer on such models were been considered in the literatures. Most techniques struggle when inter-observation times are large.

Over the last two decades, a number of epidemic models for virus spread through human population have been proposed, based on either the classical Susceptible-Infected-Removed (SIR) model developed by [6], or the classical Susceptible-Exposed –Infected-Removed (SEIR) model developed by [7].

In line with aforementioned epidemic models, this article employs Bayesian estimation approach with Stochastic Differential Equation (SDE) technique to model and estimate parameters of such models. Stochastic Differential Equation (SDE) models play prominent role in a range of application areas, including Biology, Chemistry, Epidemiology, Mechanics, Microelectronics, Economics, and Finance [8-14]. Likewise, several methods of estimating parameters in the discrete-time version of stochastic differential equations have been considered in the literature. A complete understanding of SDE theory requires familiarity with advanced probability and stochastic processes. These processes were often referred to as a diffusion process.

Diffusion processes have an advantage over some of the other stochastic formulations, in that, they can be easily derived directly from the deterministic system of ordinary differential equations and have relatively simple form [15]. Diffusion processes are a promising instrument to realistically model the time-continuous evolution of natural phenomena. To implement Diffusion

process, the best convenience idea is to introduce numerical methods of estimation via the Euler-Maruyama scheme, which employs discrete-time into continuous time models as numerical approximation. The reason for this is that most transition probabilities in diffusion processes are intractable, unless the diffusion process is analytically explicitly solvable, which are rarely the cases. Here the idea is to discretized diffusion process that would allow numerical solution approaches to solve this intractability challenges [16].

Bayesian approach to inference in the field of epidemiology had been growing in popularity over the past two decades [17]. One common approach in the literature for Bayesian estimation of diffusion models, studied independently by [12,13,18], are to consider estimating diffusion models on the basis of discrete measurements as a classic missing-data problem. The idea is to introduce augmented data points between every two consecutive observed data points so that the likelihood can be well approximated.

Generally, the idea behind Bayesian inference is that the likelihood and prior are combined using Bayes' theorem to compute the posterior distribution. Bayesian method combine prior evidence on the parameters contained in the density $\pi(\theta)$ with the likelihood $\pi(x|\theta)$ to produce the entire posterior density $\pi(\theta|x)$, from which, one may extract any information of a parameter, as in maximum likelihood estimations [19,20].

2. MATERIALS AND METHOD

Since mostly epidemic data are discretely observed, the best way to consider the dynamic of such data can be well described by discretized-version of stochastic differential equation (diffusion). Diffusion process is described as a solution to solve differential equation (Stochastic process).

The Bayesian method of estimation under diffusion process is particularly suited to discrete observed data, such as in epidemic cases, because the parameters of interest are usually defined in terms of individuals, this approach make more researchers to consider the Bayesian method of parameters estimate over the other methods of estimation. Here we can seek a numerical solution via the Euler-Maruyama approximation. The idea is to discretized the diffusion continuous model in by Euler Scheme as [16]

$$\Delta X_t \equiv X_{t+\Delta t} - X_t = \alpha(X_t,\theta)\Delta t + \beta(X_t,\theta)^{\frac{1}{2}}\Delta W_t \quad (1)$$

where $\alpha(X_t,\theta)$ denoted the drift of the model, $\beta(X_t,\theta)$ denoted the volatility of the model and ΔW_t ~ $N_d(0, I\Delta t)$ *random vector.* In (1) a small time increment Δt, result into the scheme that converged to Stochastic differential equation.

2.1 Likelihood Function

However, from the Markovian property of the diffusion, it is possible to defined the transition density from value X_{tk} at time t to X_{tk+1} at time T. Therefore, the likelihood function of the numerical solution of diffusion process (1) is of the form:

$$\underbrace{L(\theta \mid D_T)}_{Likelihood} = \prod_{k=0}^{n-1} \pi(x_{tk+1} \mid x_{tk}, \theta) \quad (2)$$

where, $\pi(x_{tk+1}|x_{tk},\theta)$ denotes the transition density of the process X_t from $X_{tk} = x_{tk}$ to $X_{tk+1} = \boldsymbol{x_{tk+1}}$.

Model transition density $\pi(\boldsymbol{x}_{tk+1}|\boldsymbol{x}_{tk},\theta)$ is not explicitly known and this is indeed a problem in the model under study. Since the maximum likelihood estimation would be intractable. We therefore considered Bayesian method of estimation.

2.2 Bayesian Inference

In statistics, Bayesian inference is a method of inference in which Bayes' rule is used to update the probability estimate for a hypothesis as additional evidence is required [19,20]. The idea behind Bayesian inference is that the likelihood and prior are combined using Bayes' theorem to compute the posterior distribution.

Bayesian method combine prior evidence on the parameters contained in the density π(θ) with the likelihood π(x|θ) to produce the entire posterior density π(θ|x) of θ. From which, one may extract any information of a parameter, as with maximum likelihood estimations.
The posterior density from (2) is given thus:

$$\underbrace{\pi(\theta \mid D_T)}_{Posterior} \propto \underbrace{\pi(\theta)}_{prior} \times \underbrace{\prod_{k=0}^{n-1} \pi^{Euler}(x_{tk+1} \mid x_{tk}, \theta)}_{Euler-density} \tag{3}$$

where π(θ) is the prior distribution of θ and the π(θ|D_T) is the posterior distribution of the parameter given observed data. The Euler-transistion density is of the form:

$$\pi^{Euler}(x_{tk+1} \mid x_{tk}, \theta) = N_d(x_{tk+1}; x_{tk} + \alpha(x_{tk}, \theta)\Delta t, \beta(x_{tk}, \theta)\Delta t) \tag{4}$$

We also adopted a data augmentation approach to fill up the low frequency gap in solve the convergence challenges uncounters in the literatures.
Under data augmentation we inserting additional m-1 time points in between times [t_{k+1},t_k]. Thus:

$$t_k = \tau_{km} < \tau_{km+1} < \cdots < \tau_{(k+1)m} = t_{k+1} \quad , \mathbf{k = 0, \ldots, K} \tag{5}$$

where $\Delta\tau = \tau_{km+1} - \tau_{km} = \dfrac{t_{k+1} - t_k}{m}$

To solve such bridge, we considered Modified Diffusion Bridge proposed by [20].
[20] assumed that the starting point ($x_0 = x_{\tau k}$) and the end point ($x_T = x_{\tau m}$) are observed.
The proposal density take the form:

$$q(x_{\tau k+1} \mid x_{\tau k}, x_T, \theta) = N(x_{\tau k+1}; x_{\tau k} + \mu(x_{\tau k}, \theta)\Delta\tau, \psi(x_{\tau k}, \theta)\Delta\tau) \tag{6}$$

Under the univariate, the Modified diffusion bridge method is of the form:

$$X_{\tau k+1} \mid x_{\tau k}, x_{\tau m} \sim N_d(\mu_{\tau k}, \psi_{\tau k}) \quad , k = 0, \ldots, m\text{-}1 \tag{7}$$

where $\mu_{\tau k} = x_{\tau k} + \dfrac{x_{\tau m} - x_{\tau k}}{\tau_m - \tau_k}\Delta\tau$ *,and* $\psi_{\tau k} = \dfrac{\tau_m - \tau_{k+1}}{\tau_m - \tau_k}\beta(x_{\tau k}, \theta)\Delta\tau$

The marginal posterior density for the imputed data π(x|$x_{\tau k}$,$x_{\tau m}$,θ) has acceptance Probability of the form:

$$\alpha(x^*_{\tau k+1}, x_{\tau k+1}) = \left\{ 1 \wedge \underbrace{\frac{\prod_{k=0}^{m} \pi(x^*_{\tau k+1} \mid x_{\tau k}, \theta)}{\prod_{k=0}^{m} \pi(x_{\tau k+1} \mid x_{\tau k}, \theta)}}_{target-distribution} \times \underbrace{\frac{\prod_{k=0}^{m-1} q(x_{\tau k+1} \mid x_{\tau k}, x_{\tau m})}{\prod_{k=0}^{m-1} q(x^*_{\tau k+1} \mid x_{\tau k}, x_{\tau m})}}_{proposal-distribution} \right\} \tag{8}$$

Therefore, the joint posterior for parameters and augmented or imputed data as the density

$$\pi(\theta, x_\tau \mid D_T) = \underbrace{\pi(\theta)}_{prior} \times \underbrace{\prod_{k=0}^{nm-1} \pi^{Euler}(x_{\tau k+1} \mid x_{\tau k}, \theta)}_{Euler-density} \quad (9)$$

In practice, the construction of a suitable proposal density could be difficult. However, for many problems of interest, it may be possible to sample from the full conditional distributions for a subset of θ as the Gibbs Sampler. We therefore adopted the sample via Markov Chain Mote Carlo (MCMC) scheme.

2.3 Markov Chain Monte Carlo (MCMC)

Markov Chain Monte Carlo (MCMC) is a very powerful tool employed to (approximately) draw samples from a specific distribution, often called the *target distribution*. Most of the MCMC algorithms used in practice satisfy the conditions which ensure convergence to the invariant distribution. From a statistical perspective, the convergence in distribution of the Markov Chain to invariant distribution is exploited to estimate expectations under the invariant measure. The acceptance Probability for the parameters is of the form:

$$\alpha(\theta^*, \theta) = \left\{1 \wedge \frac{\pi(\theta^*)\pi(x, D_T \mid \theta^*) \times q(\theta \mid \theta^*)}{\pi(\theta)\pi(x, D_T \mid \theta) \times q(\theta^* \mid \theta)}\right\} = \left\{1 \wedge \frac{\pi(\theta^*)\pi(x, D_T \mid \theta^*)}{\pi(\theta)\pi(x, D_T \mid \theta)}\right\} \quad (10)$$

Under this update scheme, the MCMC has imputed values m. Now, we alternate between draw of sampling from the parameters of interest and the imputed values. Thus, a situation where the scheme becomes degenerate should not occur.

(i) θ | w, D_T --For parameter update
(ii) w | θ, D_T -- For the innovation path update

If the full conditional distribution for the j^{th} component of θ be denoted by $\pi(\theta_j \mid \theta_1, \theta_2, \ldots, \theta_{j-1}, \theta_{j+1}, \ldots, \theta_p, D_T) = \pi(\theta_j \mid \theta_{-j}, D_T)$ $j = 1, \ldots, p$.Then, the algorithm for componentwise transitions is given by:

Algorithm 1. Metropolis-within-Gibbs sampler

1. Initialise the iteration counter to j=1 and initialise the chain with $\theta^{(0)} = (\theta_1^{(0)}, \theta_2^{(0)}, \ldots, \theta_p^{(0)})^1$

2. Obtain a new value $\theta^{(j)} = (\theta_1^{(j)}, \theta_2^{(j)}, \ldots, \theta_p^{(j)})^1$ *from* $\theta^{(j-1)}$ *by successive generation of values*

$\theta_1^{(j)} \sim \pi(\theta_1 \mid \theta_2^{(j-1)}, \cdots, \theta_p^{(j-1)}, D_T)$ *Using a Metropolis-Hastings step with proposal* $q_1(\theta_1^* \mid \theta_1^{i-1})$

$\theta_2^{(j)} \sim \pi(\theta_2 \mid \theta_1^{(j)} \theta_3^{(j-1)}, \cdots, \theta_p^{(j-1)}, D_T)$ *Using a Metropolis-Hastings step with proposal* $q_2(\theta_2^* \mid \theta_2^{i-1})$

$\vdots$

$\theta_p^{(j)} \sim \pi(\theta_p \mid \theta_1^{(j)}, \theta_2^{(j)}, \cdots, \theta_{p-1}^{(j)}, D_T)$ *Using a Metropolis-Hastings step with proposal* $q_p(\theta_p^* \mid \theta_p^{i-1})$

3. Change counters j to j+1, and return to step 2.

If the full conditional distribution for the j^{th} component of θ is available to sample from directly, the resulting acceptance probability is one.

2.4 Convergence

One way of testing the convergence is to see a well chain mixing or moving around the parameter space. Trace plots document the magnitude of the sample drawn (y-axis) at each iteration (x-axis) of the Markov Chain Monte Carlo (MCMC) procedure. Once the chain has identified the stationary distribution of samples, the samples that are drawn will appear to have been randomly sampled from the same region of the y-axis. The below are the results of well and bad convergence.

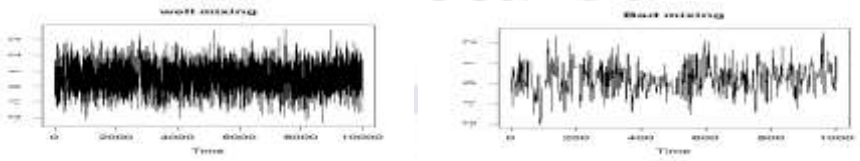

Figure 1. *Well mixing trace plot (Stationary) and bad mixing trace plot*

2.5 Epidemic Model

We implored the stochastic SEIR epidemic model for infectious disease that based on three dimensional processes, with the first component S_t represents the susceptible individuals, the second component E_t represents the exposed individuals and the third component I_t represents the infection individual infected at time t.
Therefor, the Diffusion SEIR Epidemic Model is of the form:

$$\begin{pmatrix} ds_t \\ de_t \\ di_t \end{pmatrix} = \begin{pmatrix} -\beta N s_t i_t \\ \beta N s_t i_t - \gamma e_t \\ \gamma e_t - \alpha i_t \end{pmatrix} dt + \begin{pmatrix} -\frac{1}{N}\sqrt{\beta N s_t i_t} & 0 & 0 \\ \frac{1}{N}\sqrt{\beta N s_t i_t} & -\frac{1}{N}\sqrt{\gamma N e_t} & 0 \\ 0 & \frac{1}{N}\sqrt{\gamma N e_t} & -\frac{1}{N}\sqrt{\alpha N i_t} \end{pmatrix} \begin{pmatrix} dW_{1t} \\ dW_{2t} \\ dW_{3t} \end{pmatrix} \quad (11)$$

3. RESULTS AND DISCUSSIONS

We demonstrate the performance of aforementioned methods by simulation approach on the stochastic SEIR epidemic model for infectious diseases based on three dimensional diffusion process with drift and diffusion coefficient parameterised proposed in [22].
The state variable $X_t = (s, e, i)^T$, where, s represents the susceptible individuals, e represent exposed individuals, and i represent the infection component of individuals infected.

3.1 Simulation

We let the initial conditions of this state variables values $X_0 = (5363500, 1, 25)^T$ respectively. From the model (11), the parameter of interest denoted by $\boldsymbol{\theta = (\beta, \gamma, \alpha)^T}$.
With initialised the parameters of the sampler with $\mathbf{0 < \beta < 1}$, $\mathbf{0 < \gamma < 0.7}$ and $\mathbf{0.1 < \alpha < 1}$ for the randomness of the transmission rate $\boldsymbol{\beta}$, exposed rate $\boldsymbol{\gamma}$ and infection rate $\boldsymbol{\alpha}$ respectively.
The iterations were performed for 10^3 and 10^4 using Metropolis-Within- Gibbs sampler. With the different number of imputed time points of $\boldsymbol{m = 5}$, $\boldsymbol{m = 15}$ and $\boldsymbol{m = 50}$. We considered independently distribution for the proposal of parameter of interest $N_d(0, \psi_j^2)$, where ψ_j^2 is the chosen variance, turning until we have $(0.009, 0.009, 0.001)^T$.
We choose an uninformative prior for each of the parameter, and apply the MCMC scheme to infer the posterior values of the model.

To show that the method does not degenerate when increasing the number of imputed time points. We set the starting time point at $t_0 = 0$ and end-time at $T = 30$, with equidistant time interval $\Delta\tau = 0.001$. And the results were depicted below.

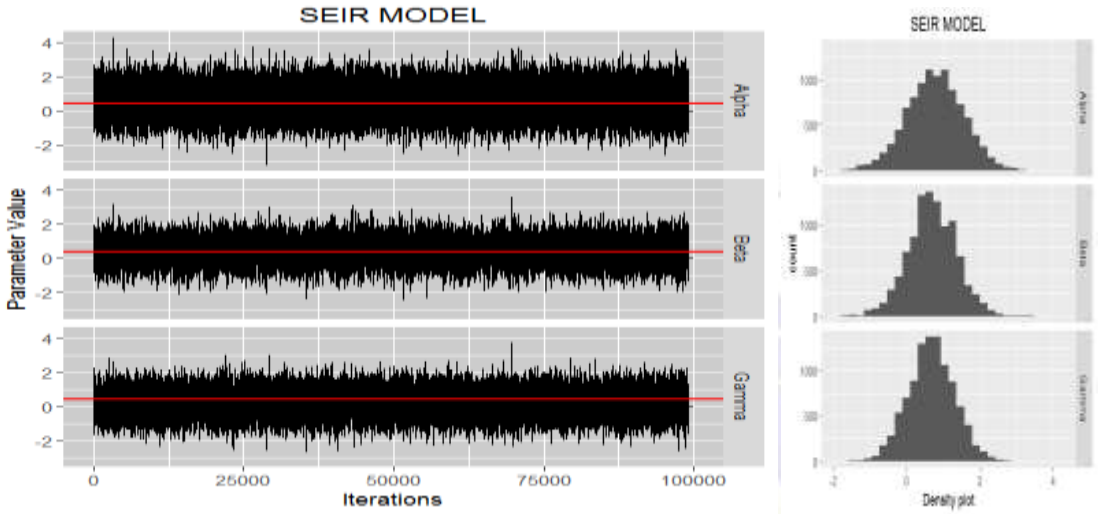

Figure 2. The trace plot and the density plot for the three parameters

Figure 2(a) shows the trace plot for the three parameters, the trace plot mixing very well. And (b) shows the density plot for the modified innovation scheme for three different imputed values, the three imputed were very closed.

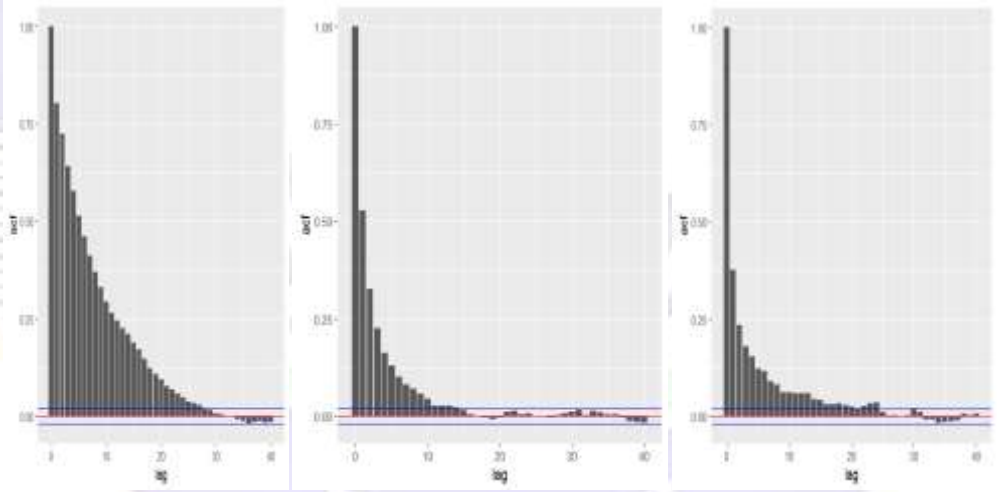

Figure 3. *Shows the result of Autocorrelation plot*

The results obtained from posterior distribution when the number of imputed points increases does not worsen the mixing of the chain as was see in auto-correlation curve in figure 3.

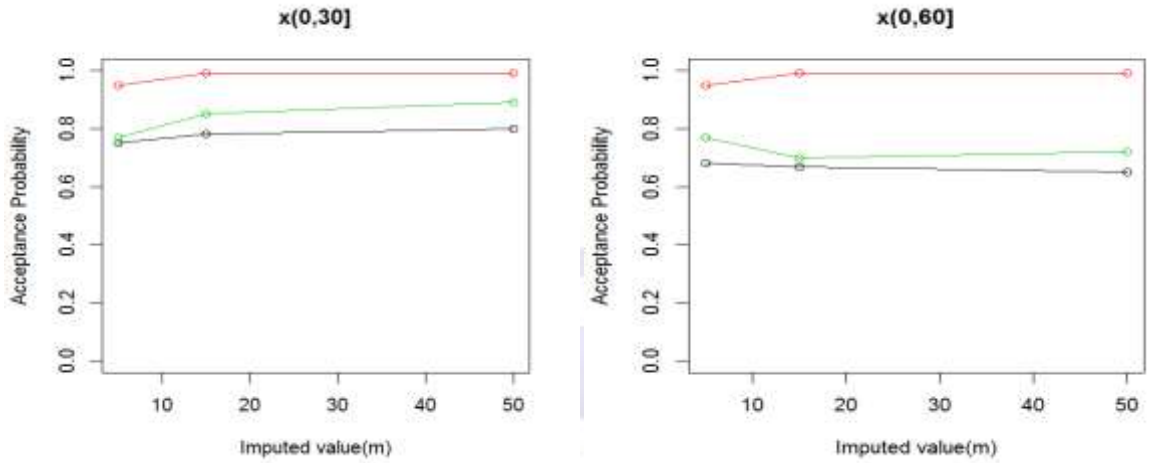

Figure 4. *Shows the Acceptance probability plot for the three parameters*

Figure 4. Shows the Acceptance probability for Modified Innovation Scheme method of path update for three different value of imputed observation time (red = Modified Diffusion Bridge, green = Diffusion Bridge and the black represent the Euler proposal). We have both parameters and path update that were consistent. Likewise, the situation where the scheme becomes degenerate does not occur.

4. CONCLUSIONS

Most epidemic data are discretely observed and undergo stochastic transition rate. The frequentist based method of inference can be problematic, as the transition densities were rarely available in closed form. This article contributes to stochastic epidemic modeling using diffusion approximation approach as well as Bayesian data-augmentation statistical estimation in discretely observed diffusion processes. The utilisation of diffusion approximations, coupled with Bayesian inference techniques in the modeling of the spread of infectious diseases (epidemic models), is new. There are few amount of literature regarding, diffusion epidemic models. The extensive simulation study revealed that satisfactory estimation results for the parameters of interest were obtained. The combined application of diffusion epidemic modeling and Bayesian inference, promises to supply new insights in many exciting areas of natural phenomena in the future.

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